



MET SER LEU LEU THR GLU VAL GLU THR PRO ILE  
ATGAGCCTTCTAACCGAGGTCGAAAC . . . ACCTAT  
TACTCGGAAGATTGGCTCCAGCTTTG . . . TGGATA  
10 20 720

ARG ASN GLU TRP GLU CYS ARG CYS ASN GLY  
CAGAAACGAATGGGAGTGCA GATGCAACGG  
GTCTTTTGCTTACCCTCACGTCTACGTTGCC  
730 740 750

SER SER ASP PRO LEU VAL VAL ALA ALA SER  
TTCAAGTGAC CCGCTTGTTGTGCTGCGAG  
AAGTTCACTG GCGGAACAACAACGACGCTC  
760 770 780

ILE ILE GLY ILE LEU HIS LEU ILE LEU TRP  
TATCATTTGGGATCTTGCACTTGATATTGTG  
ATAGTAACCTAGAACGTGAACATAAACAC  
790 800 810

ILE PHE ASP ARG LEU PHE PHE LYS CYS ILE  
GATTTTT GATCGTCTTTTTTTTCAAATGCAT  
CTAAAAA CTAGCAGAAAAAAGTTTACGTA  
820 830 840

TYR ARG LEU PHE LYS TYR GLY LEU LYS ARG  
CTATCGACTCTTCAAATACGGTCTGAAAAAG  
GATAGCTGAGAAGTTTATGCCAGACTTTTC  
850 860 870

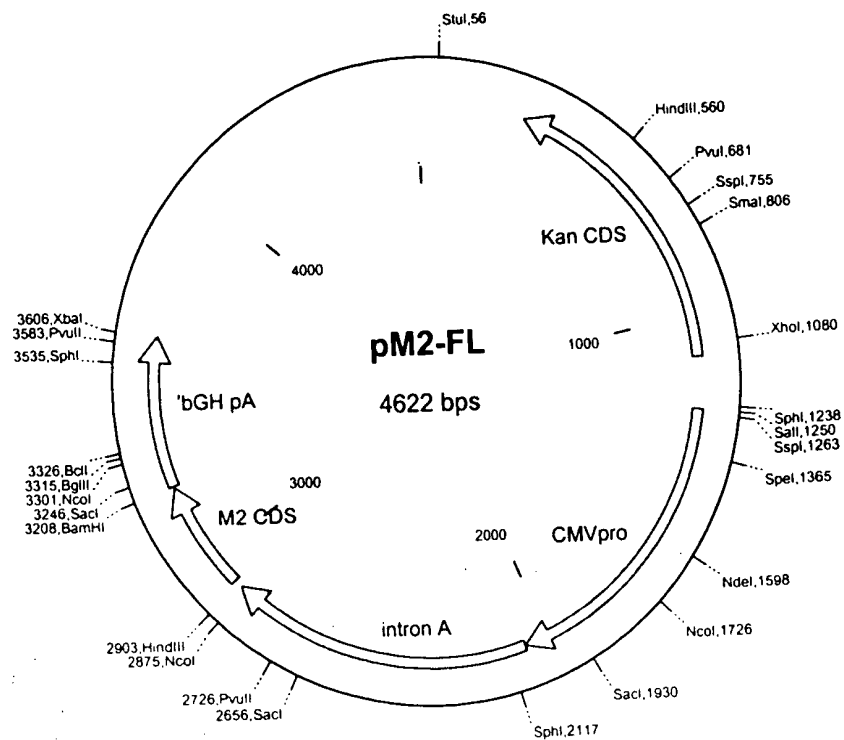
GLY PRO SER THR GLU GLY VAL PRO GLU SER  
AGGGCCTTCTACGGGAAGGAGTACCTGAGTC  
TCCCGGAAGATGCCTTCTCATGGACTCAG  
880 890 900

MET ARG GLU GLU TYR ARG LYS GLU GLN GLN  
TATGAGGGAAGAAATATCGAAAGGAACAGCA  
ATACTCCCTTCTTAGCTTTTCCTTGTCTG  
910 920 930

ASN ALA VAL ASP ALA ASP ASP SER HIS PHE  
GAATGCTGTGGATGCTGACGACAGTCAATTT  
CTTACGACACCTACGACTGCTGTCAATAA  
940 950 960

VAL SER ILE GLU LEU GLU \*\*\*  
TGTCAGCATAGAGCTGGAGTAA  
ACAGTCTGATCTCGACCTCATTT  
970 980

Figure 2



**Figure 3**

1 GGGGGGGGGG GCGCTGAGG TCTGCCTCGT GAAGAAGGTG TTGCTGACTC ATACCAGGCC TGAATCGCCC CATCATCCAG CCAGAAAGTG  
91 AGGGAGCCAC GGTGTATGAG AGCTTTGTTG TAGGTGGACC AGTTGGTGAT TTTGAACTTT TGCTTTGCCA CGGAACGGTC TGCCTTGTGCG  
181 GGAAGATGCG TGATCTGATC CTTCAACTCA GCAAAAGTTC GATTATTCA ACAAAGCGC CGTCCCGTCA AGTCAGCGTA ATGCTCTGCC  
271 AGTGTTACAA CCAATTAACC AATTCTGATT AGAAAACTC ATCGAGCATC AAATGAACT GCAATTTATT CATATCAGGA TTATCAATAC  
<<.....Kan CDS.....>>  
361 CATATTTTGG AAAAGCCGT TTCTGTAATG AAGGAGAAAA CTCACCGAGG CAGTTCCATA GGATGGCAAG ATCCTGGTAT CGGTCTGCGA  
<.....Kan CDS.....>  
451 TTCCGACTCG TCCAACATCA ATACAACCTA TTAATTTCCC CTCGTCAAAA ATAAGGTTAT CAAGTGAGAA ATCACCATGA GTGACGACTG  
<.....Kan CDS.....>  
541 AATCCGGTGA GAATGGCAAA AGCTTATGCA TTTCTTTCCA GACTTGTTC ACAGGCCAGC CATTACGCTC GTCATCAAAA TCACTCGCAT  
<.....Kan CDS.....>  
631 CAACCAAACC GTTATTCATT CGTGATTGCG CTGAGCGAG ACGAAATACG CGATCGCTGT TAAAAGGACA ATTACAAACA GGAATCGAAT  
<.....Kan CDS.....>  
721 GCAACCGGCG CAGGAACACT GCCAGCGCAT CAACAATATT TTCACCTGAA TCAGGATATT CTCTAATAC CTGGAATGCT GTTTTCCCGG  
<.....Kan CDS.....>  
811 GGATCGCAGT GGTGAGTAAC CATGCATCAT CAGGAGTACG GATAAAATGC TTGATGGTGC GAAGAGGCAT AAATCCGTC AGCCAGTTTA  
<.....Kan CDS.....>  
901 GTCTGACCAT CTCATCTGTA ACATCATTGG CAACGCTACC TTTGCCATGT TTCAGAAACA ACTCTGGCGC ATCGGGCTTC CCATACAATC  
<.....Kan CDS.....>  
991 GATAGATTGT CGCACCTGAT TGCCCGACAT TATCGCGAGC CCATTATAC CCATATAAAT CAGCATCCAT GTTGGAATTT AATCGCGGCC  
<.....Kan CDS.....>  
1081 TCGAGCAAGA CGTTTCCCGT TGAATATGGC TCATAACACC CTTGTATTA CTGTTTATGT AAGCAGACAG TTTTATTGTT CATGATGATA  
<.....Kan CDS.....>  
1171 TATTTTATC TTGTGCAATG TAACATCAGA GATTTTGAGA CACAACGTGG CTTTCCCCC CCCCCCGCA TGCCTGCAGG TCGACATAAA  
>>CMVpro.>  
1261 TCAATATTGG CTATTGGCCA TTGCATACGT TGTATCTATA TCATAATATG TACATTTATA TTGGCTCATG TCCAATATGA CCGCATGTT  
>.....CMVpro.....>  
1351 GACATTGATT ATTGACTAGT TATTAATAGT AATCAATTAC GGGGTCATTA GTTCATAGCC CATATATGGA GTTCCGCGTT ACATAACTTA  
>.....CMVpro.....>  
1441 CGGTAAATGG CCCGCTCGT GACCGCCCAA CGACCCCGC CCATTGACGT CAATAATGAC GTATGTTCCC ATAGTAACGC CAATAGGGAC  
>.....CMVpro.....>  
1531 TTTCATTGA CGTCAATGGG TGGAGTATTT ACGGTAACT GCCCACTGG CAGTACATCA AGTGTATCAT ATGCCAAGTC CGGCCCTTA  
>.....CMVpro.....>  
1621 TTGACGTCAA TGACGGTAAA TGGCCCGCT GGCATTATGC CCAGTACATG ACCTTACGGG ACTTTCCTAC TTGGCAGTAC ATCTACGTAT  
>.....CMVpro.....>  
1711 TAGTCATCGC TATTACCATG GTGATGCGT TTTGGCAGTA CACCAATGGG CGTGATAGC GGTTTGACTC ACGGGGATT CCAAGTCTCC  
>.....CMVpro.....>  
1801 ACCCCATTGA CGTCAATGGG AGTTTGTITT GGCACCAAAA TCAACGGGAC TTCCAAAAT GTCGTAATAA CCCCCCGCG TTGACGCAAA  
>.....CMVpro.....>

1891 TGGGCGGTAG GCGTGACGG TGGGAGGTCT ATATAAGCAG AGCTCGTTTA GTGAACCGTC AGATCGCCTG GAGACGCCAT CCACGCTGTT  
>.....CMVpro.....>

1981 TTGACCTCCA TAGAAGACAC CGGACCGAT CCAGCCTCCG CGGCCGGAA CGGTGCATTG GAACGCGGAT TCCCGTGCC AAGAGTGACG  
>.....CMVpro.....>

2071 TAAGTACCGC CTATAGACTC TATAGGCACA CCCCTTTGGC TCTTATGCAT GCTATACTGT TTTTGGCTTG GGGCCTATAC ACCCCGCTC  
>.....intron A.....>

2161 CTTATGCTAT AGGTGATGGT ATAGCTTAGC CTATAGGTGT GGGTTATTGA CCATTATTGA CCACTCCCCT ATTGGTGACG ATACTTTCCA  
>.....intron A.....>

2251 TTACTAATCC ATAACATGGC TCTTTGCCAC AACTATCTCT ATTGGCTATA TGCCAATACT CTGTCCTTCA GAGACTGACA CGGACTCTGT  
>.....intron A.....>

2341 ATTTTACAG GATGGGTCC CATTATTAT TTACAAATC ACATATACAA CAACGCGTC CCCCCTGCC GAGTTTTTA TTAACATAG  
>.....intron A.....>

2431 CGTGGGATCT CCACGGAAT CTCGGGTACG TGTTCGGAC ATGGGCTCTT CTCGGTAGC GCGGAGCTT CCACATCCGA GCCCTGGTCC  
>.....intron A.....>

2521 CATGCTCCA GCGCTCATG GTCGCTCGG AGCTCCTGC TCCTAACAGT GGAGGCCAGA CTTAGGCACA GCACAATGCC CACCACCAC  
>.....intron A.....>

2611 AGTGTGCGC ACAAGCCGT GCGGTAGGG TATGTGCTG AAAATGAGCT CGGAGATTG GTCGCACCG TGACGCAGAT GGAAGACTTA  
>.....intron A.....>

2701 AGGCAGCGC AGAAGAAGAT GCAGGCAGT GAGTTGTTT ATTCTGATA GAGTCAGAG TAACTCCCGT TGCGGTGCTG TTAACGGTG  
>.....intron A.....>

2791 AGGCAGTGT AGTCTGACG GTACTGTTG CTGCGCGCG CGCCACCAGA CATAATAGCT GACAGACTAA CAGACTGTTT CTTTCCATG  
>.....intron A.....>

2881 GTCTTTCTG CAGTCACCG CCAAGCTTC ACCATGAGC TTCTAACGA GGTGAAACA CCTATCAGAA ACGAATGGGA GTGCAGATG  
>>.....M2 CDS.....>>  
>.....intron A.....>

2971 AACGGTTCAA GTGACCCGCT TGTGTTGCT GCGAGTATCA TTGGATCTT GCACTTGATA TTGTGGATT TTGATCGTCT TTTTTCAAA  
>.....M2 CDS.....>

3061 TGCATCTATC GACTCTTCAA ATACGGTCTG AAAAGAGGGC CTTCTACGA AGGAGTACCT GAGTCTATGA GGAAGAATA TCGAAAGGAA  
>.....M2 CDS.....>

3151 CAGCAGAATG CTGTGGATG TGACGACAGT CATTGTTGCA GCATAGAGCT GGAGTAAGGA TCCTCGCAAT CCCTAGGAGG ATTAGGCAAG  
>>.....'bGH pA.....>>  
>.....M2 CDS.....>>

3241 GGCTTGAGCT CAGCTCTTG TGAGGGACAG AAATACAATC AGGGGCAGTA TATGAATACT CCATGGAGAA ACCCAGATCT ACGTATGATC  
>.....'bGH pA.....>

3331 AGCCTCGACT GTGCCCTTA GTTGCCAGCC ATCTGTTGT TGCCCCCTCC CCGTGCCTC CTGACCCCTG GAAGTGCCA CTCCCACTGT  
>.....'bGH pA.....>

3421 CTTTCTTAA TAAATGAGG AAATTGATC GCATTGCTG AGTAGGTGC ATTCTATTCT GGGGGTGGG GTGGGCGAGG ACAGCAAGG  
>.....'bGH pA.....>

3511 GGAGGATTG GAAGACAATA GCAGCATGC TGGGGATCG GTGGGCTTA TGGCTTCTGA GCGGAAAGA ACCAGCTGG GCTCGACAGC  
>.....'bGH pA.....>

3601 TGAAGTCTA AATGCTTCC TCGCTACTG ACTCGCTGCG CTCGGTCTT CGGCTCGGC GAGCGGTATC AGCTCACTCA AAGGCGGTAA  
>.....'bGH pA.....>>

3691 TACGGTTATC CACAGAATCA GGGGATAACG CAGGAAAGAA CATGTGAGCA AAAGGCCAGC AAAAGGCCAG GAACCGTAAA AAGGCCGCGT  
3781 TGCTGGCGTT TTTCCATAGG CTCCGCCCCC CTGACGAGCA TCACAAAAAT CGACGCTCAA GTCAGAGGTG GCGAAACCCG ACAGGACTAT  
3871 AAAGATACCA GGC GTTTTCCC CTGGAAGCT CCTCGTGGC CTCTCTGTT CCGACCTGC CGCTTACCGG ATACCTGTCC GCCTTTCTCC  
3961 CTTCCGGAAG CGTGGCGCTT TCTCAATGCT CACGCTGTAG GTATCTCAGT TCGGTGTAGG TCGTTCGCTC CAAGCTGGGC TGTGTGCAG  
4051 AACCCCCCGT TCAGCCCGAC CGTGGCGCT TATCCGTAA CTATCGTCTT GAGTCCAACC CGGTAAGACA CGACTTATCG CCACTGGCAG  
4141 CAGCCACTGG TAACAGGATT AGCAGAGCGA GGTATGTAGG CGGTGCTACA GAGTTCTTGA AGTGGTGGCC TAACTACGGC TACTAGAA  
4231 GGACAGTATT TGGTATCTGC GCTCTGCTGA AGCCAGTTAC CTTCCGAAAA AGAGTTGGTA GCTCTTGATC CGGCAACAA ACCACCGTG  
4321 GTAGCGGTGG TTTTTTGTG TGCAAGCAGC AGATTACGG CAGAAAAAAA GGATCTCAAG AAGATCCTTT GATCTTTTCT ACGGGGTCTG  
4411 ACGCTCAGTG GAACGAAAAC TCACGTTAAG GGATTTTGGT CATGAGATTA TCAAAAAGGA TCTTCACCTA GATCCTTTTA AATTAATAAT  
4501 GAAGTTTTAA ATCAATCTAA AGTATATATG AGTAACTTG GTCTGACAGT TACCAATGCT TAATCAGTGA GGCACCTATC TCAGCGATCT  
4591 GTCTATTTG TTCATCCATA GTGCCTGAC TC

Figure 4

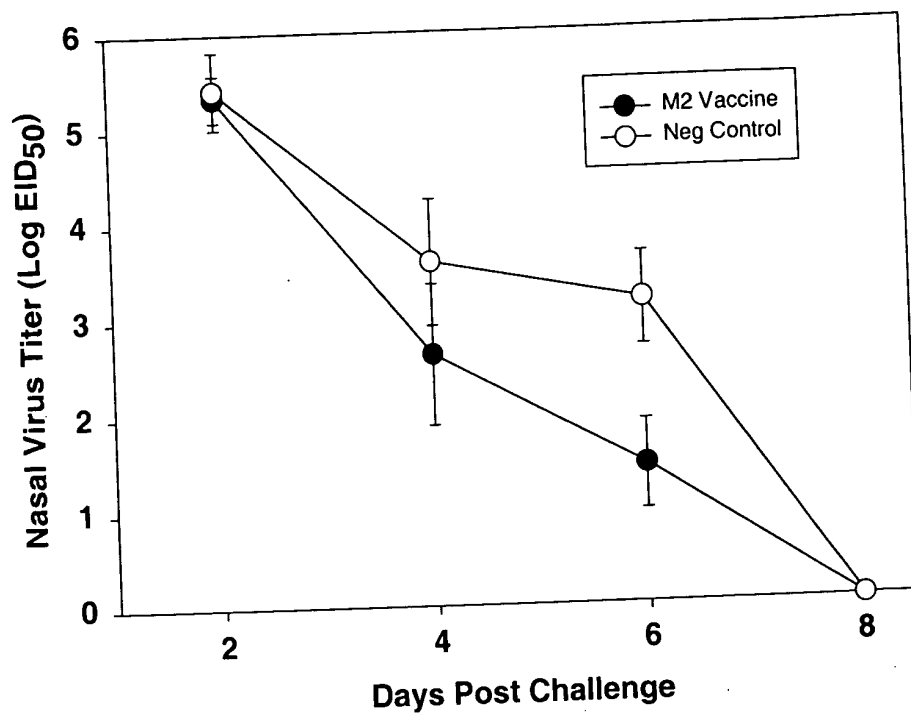


Figure 5